



BLAST

NCBI's sequence similarity search tool designed to support analysis of nucleotide and protein databases.

Overview

NEW The Old (ungapped) BLAST service has been moved to the bottom of the page. NCBI recommends the use of BLAST 2.0 (Gapped BLAST), as this is a newer, improved service.

BLAST FAQs

BLAST 2.0

New/Noteworthy

NEW PHI-
BLAST

- [Basic BLAST search](#)
- [Advanced BLAST search](#)

Manual

Position Specific Iterated BLAST

- [PSI-BLAST search](#)

NCBI Home

NEW Pattern Hit Initiated BLAST

NLM Home

- [PHI-BLAST search](#)

NIH Home

NEW BLAST 2 sequences against each other

- [BLAST 2 sequences](#)

Credits

Specialized BLAST pages

- [Unfinished microbial genomes](#) NEW
- [P. falciparum](#)
- [TIGR Tentative Human Consensus \(THC\) sequences](#)

Old (ungapped) BLAST page

- [Ungapped BLAST search](#)



Exhibit C

General NCBI information: <info@ncbi.nlm.nih.gov>

BLAST questions: <blast-help@ncbi.nlm.nih.gov>

NCBI	Advanced BLAST		Entrez	?
<input type="button" value="Clear Input"/>		<input type="button" value="Basic BLAST"/>		
 Message of the day .. Gapped BLAST <i>(BLAST version 2.0) is now available!</i>		Choose program to use and database to search: Program <input type="text" value="blastp"/> Database <input type="text" value="nr"/>		

The query sequence is filtered for low complexity regions by default.

Depending on server load your search may take several seconds to several minutes.
 Note: Nothing will be returned until your search is complete.

Enter here your input data as	<input type="text" value="Sequence in FASTA format"/>	<input type="button" value="Submit Query"/>
<pre>ssqyrgvtfyrrtgrweshiwdcgkqvylggfdtahaaaraydraaikfrgveadinfni ddyddd1</pre>		

Please read about FASTA format description

Advanced options for the BLAST server:

Expect	<input type="text" value="default"/>	Cutoff	<input type="text" value="default"/>	Matrix	<input type="text" value="default"/>
Strand	<input type="text" value="both"/>	Filter	<input type="text" value="none"/>	<input type="checkbox"/> Histogram	<input type="checkbox"/> NCBI-gi
Descriptions	<input type="text" value="default"/>	Alignments	<input type="text" value="default"/>		

Other advanced options:

<input type="checkbox"/> Send reply to the Email address:	<input type="text"/>	<input type="checkbox"/> In HTML format
<input type="button" value="Submit Query"/>		

Comments and suggestions to: <blast-help@ncbi.nlm.nih.gov>

Credits to: [Sergei B. Shavirin](#)

Acknowledgements to: [Tom Madden](#) and [Jonathan Epstein](#)

NCBI

BLAST Search Results

Entrez ?

Your query has been submitted, please wait for results

BLASTP 1.4.11 [24-Nov-97] [Build 24-Nov-97]

Reference: Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J. Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Query= tmpseq_1
(67 letters)

Database: Non-redundant GenBank CDS
translations+PDB+SwissProt+SPupdate+PIR
331,304 sequences; 101,007,400 total letters.

Searching.....done

			Smallest Sum		
			High Score	Probability P(N)	N
Sequences producing High-scoring Segment Pairs:					
<u>sp P47927 AP2_ARATH</u>	FLORAL HOMEOATIC PROTEIN APETALA2 /gi...	<u>368</u>	<u>1.1e-43</u>	<u>1</u>	
<u>gi 2944040</u>	(AF048900) indeterminate spikelet 1 ...	<u>345</u>	<u>1.9e-40</u>	<u>1</u>	
<u>gi 2281639</u>	(AF003100) AP2 domain containing pro...	<u>340</u>	<u>9.5e-40</u>	<u>1</u>	
<u>gi 1732031</u>	(U41466) AP2 DNA-binding domain prot...	<u>327</u>	<u>6.4e-38</u>	<u>1</u>	
<u>gi 3402680</u>	(AC004697) putative floral homeotic ...	<u>319</u>	<u>8.5e-37</u>	<u>1</u>	
<u>gi 2098818</u>	(AF001012) GLOSSY15 [Zea mays]	<u>205</u>	<u>9.0e-21</u>	<u>1</u>	
<u>gi 2887500</u>	(AC002339) putative AP2 domain-conta...	<u>126</u>	<u>1.3e-16</u>	<u>2</u>	
<u>pir S71365</u>	AP2 domain-containing protein - Arab...	<u>116</u>	<u>6.6e-16</u>	<u>2</u>	
<u>gi 1171429</u>	(U44028) CKC [Arabidopsis thaliana]	<u>116</u>	<u>6.6e-16</u>	<u>2</u>	
<u>gnl PID e1188628</u>	(Z47554) orf [Zea mays]	<u>123</u>	<u>3.2e-15</u>	<u>2</u>	
<u>pir S54116</u>	hypothetical protein - maize	<u>123</u>	<u>3.0e-09</u>	<u>1</u>	
<u>gi 2281641</u>	(AF003101) AP2 domain containing pro...	<u>112</u>	<u>1.1e-07</u>	<u>1</u>	
<u>gi 2281637</u>	(AF003099) AP2 domain containing pro...	<u>110</u>	<u>2.0e-07</u>	<u>1</u>	
<u>gnl PID d1007901</u>	(D38125) EREBP-4 [Nicotiana tabacum]	<u>110</u>	<u>2.0e-07</u>	<u>1</u>	
<u>gi 3617742</u>	(AC005687) RAP2.6 [Arabidopsis thali...	<u>110</u>	<u>2.0e-07</u>	<u>1</u>	
<u>gi 1903358</u>	(AC000104) Similar to Nicotiana EREB...	<u>106</u>	<u>7.4e-07</u>	<u>1</u>	
<u>gnl PID d1033384</u>	(AB008107) ethylene responsive eleme...	<u>105</u>	<u>1.0e-06</u>	<u>1</u>	
<u>gi 2529675</u>	(AC002535) putative AP2 domain conta...	<u>101</u>	<u>1.1e-06</u>	<u>2</u>	
<u>gi 2281635</u>	(AF003098) AP2 domain containing pro...	<u>100</u>	<u>2.7e-06</u>	<u>2</u>	
<u>gnl PID d1033383</u>	(AB008106) ethylene responsive eleme...	<u>100</u>	<u>2.8e-06</u>	<u>2</u>	
<u>gi 1707016</u>	(U78721) cadmium-induced protein iso...	<u>101</u>	<u>3.7e-06</u>	<u>1</u>	
<u>gi 2281629</u>	(AF003095) AP2 domain containing pro...	<u>101</u>	<u>3.7e-06</u>	<u>1</u>	
<u>gi 2213783</u>	(U89256) Pt15 [Lycopersicon esculentum]	<u>100</u>	<u>5.1e-06</u>	<u>1</u>	
<u>gnl PID d1007900</u>	(D38124) EREBP-3 [Nicotiana tabacum]	<u>97</u>	<u>7.3e-06</u>	<u>2</u>	
<u>gi 1732406</u>	(U81157) S25-XP1 DNA binding protein...	<u>98</u>	<u>9.8e-06</u>	<u>1</u>	
<u>gi 3600050</u>	(AF080120) contains similarity to AP...	<u>95</u>	<u>1.3e-05</u>	<u>2</u>	
<u>gnl PID d1032484</u>	(AB013301) ethylene responsive eleme...	<u>97</u>	<u>1.4e-05</u>	<u>1</u>	
<u>gnl PID d1033382</u>	(AB008105) ethylene responsive eleme...	<u>97</u>	<u>1.4e-05</u>	<u>1</u>	
<u>gnl PID e327065</u>	(Z97343) EREBP-4 homolog [Arabidopsi...	<u>97</u>	<u>1.4e-05</u>	<u>1</u>	
<u>gi 2213785</u>	(U89257) Pt16 [Lycopersicon esculentum]	<u>95</u>	<u>1.5e-05</u>	<u>2</u>	
<u>gi 2281649</u>	(AF003105) AP2 domain containing pro...	<u>96</u>	<u>1.9e-05</u>	<u>1</u>	
<u>gnl PID d1033380</u>	(AB008103) ethylene responsive eleme...	<u>96</u>	<u>1.9e-05</u>	<u>1</u>	
<u>gi 3342211</u>	(U89255) Pt14 [Lycopersicon esculentum]	<u>93</u>	<u>4.9e-05</u>	<u>1</u>	

<u>gi 3264767</u>	(AF071893) AP2 domain containing pro...	93	4.9e-05	1
<u>gi 3065895</u>	(AF058827) TSI1 [Nicotiana tabacum]	91	5.4e-05	2
<u>gi 1688233</u>	(U77655) DNA binding protein homolog...	74	8.0e-05	3
<u>gnl PID d1007902</u>	(D38126) EREBP-2 [Nicotiana tabacum]	91	9.5e-05	1
<u>gi 2344900</u>	(AC002388) EREBP isolog [Arabidopsis...	90	0.00013	1
<u>gi 2281633</u>	(AF003097) AP2 domain containing pro...	90	0.00013	1
<u>gnl PID d1033381</u>	(AB008104) ethylene responsive eleme...	88	0.00025	1
<u>gnl PID e1287891</u>	(AL022605) putative protein [Arabido...	88	0.00025	1
<u>gnl PID e353340</u>	(AJ001911) putative Ckc2 [Arabidopsi...	88	0.00025	1
<u>gi 2281631</u>	(AF003096) AP2 domain containing pro...	87	0.00034	1
<u>gnl PID d1007899</u>	(D38123) ERF1 [Nicotiana tabacum]	87	0.00034	1
<u>gnl PID e1283534</u>	(AL022197) transcriptional activator...	82	0.00039	2
<u>gi 1899058</u>	(U77378) transcriptional activator C...	82	0.00039	2
<u>gi 2281643</u>	(AF003102) AP2 domain containing pro...	86	0.00048	1
<u>gnl PID e1249610</u>	(AL021710) EREBP - like protein [Ara...	85	0.00066	1
<u>gnl PID e353195</u>	(Z99707) APETALA2 domain containing ...	83	0.00066	2
<u>gi 2281647</u>	(AF003104) AP2 domain containing pro...	81	0.00090	2
<u>gnl PID d1034402</u>	(AB013817) DREB1C [Arabidopsis thali...	84	0.00091	1
<u>gnl PID e1283536</u>	(AL022197) transcriptional activator...	84	0.00091	1
<u>gi 2642430</u>	(AC002391) putative AP2 domain conta...	81	0.0011	2
<u>gi 2281645</u>	(AF003103) AP2 domain containing pro...	83	0.0013	1
<u>gnl PID d1034763</u>	(AB007787) DREB1A [Arabidopsis thali...	82	0.0017	1
<u>gnl PID d1034400</u>	(AB013815) DREB1A [Arabidopsis thali...	82	0.0017	1
<u>sp P42736 CD13_ARATH</u>	CADMIUM-INDUCED PROTEIN AS30 /pir S...	82	0.0017	1
<u>gnl PID e1283535</u>	(AL022197) transcriptional activator...	82	0.0017	1
<u>gi 3702318</u>	(AC005397) putative Ap2 domain prote...	81	0.0024	1
<u>gnl PID e1283544</u>	(AL022198) putative protein [Arabido...	81	0.0024	1
<u>gi 3643601</u>	(AC005395) hypothetical protein [Ara...	80	0.0033	1
<u>gi 3540200</u>	(AC004260) Similar to TINY [Arabidop...	79	0.0046	1
<u>gi 3282693</u>	(AF040959) AP2 domain family transcr...	79	0.0046	1
<u>gi 2213612</u>	(AC000103) F21J9.6 [Arabidopsis thal...	79	0.0046	1
<u>gi 2281627</u>	(AF003094) AP2 domain containing pro...	74	0.0076	2
<u>gi 2344890</u>	(AC002388) TINY transcription factor...	77	0.0087	1
<u>gi 3395438</u>	(AC004683) putative AP2 domain conta...	76	0.012	1
<u>gi 2062174</u>	(AC001645) transcription factor (TIN...	76	0.012	1
<u>gnl PID d1034766</u>	(AB007790) DREB2A [Arabidopsis thali...	75	0.017	1
<u>gnl PID d1034767</u>	(AB007791) DREB2B [Arabidopsis thali...	75	0.017	1
<u>gnl PID e218696</u>	(X94698) TINY [Arabidopsis thaliana]...	73	0.032	1
<u>gi 3695034</u>	(AF057373) ethylene response element...	72	0.043	1
<u>sp P16146 PZ02_LUPPO</u>	PPLZ02 PROTEIN /pir S11881 hypothet...	68	0.15	1
<u>gi 47216</u>	(X52071) unidentified product (195 A...	61	0.79	1
<u>gi 485957</u>	(Z32686) mrpD gene product [Proteus ...	58	0.98	1
<u>gi 3033545</u>	(AF055873) lignostilbene-alpha,beta-...	47	0.998	2
<u>sp P34114 PHS2_DICDI</u>	GLYCOGEN PHOSPHORYLASE 2 (GP2) /pir ...	56	0.9996	1
<u>gi 2065531</u>	(U78526) endo-1,4-beta-glucanase [Ly...	56	0.9996	1
<u>sp P32932 VNS2_BTV1S</u>	NONSTRUCTURAL PROTEIN NS2 /pir JC12...	56	0.9996	1
<u>gnl PID d1021365</u>	(D86222) glutamine synthetase [Pyroc...	56	0.9996	1

sp|P47927|AP2_ARATH FLORAL HOMEOTIC PROTEIN APETALA2 gi|533709 (U12546)
 APETALA2 protein [Arabidopsis thaliana] gnl|PID|e353193 (Z99707)
 APETALA2 protein [Arabidopsis thaliana]
 Length = 432

Score = 368 (171.8 bits), Expect = 1.1e-43, P = 1.1e-43
 Identities = 67/67 (100%), Positives = 67/67 (100%)

Query: 1 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDATAAAARAYDRAAIKFRGVEADINFNI 60
 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDATAAAARAYDRAAIKFRGVEADINFNI

Subject: 129 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAARAYDRAAIKFRGVEADINFNI 188

Query: 61 DDYDDDL 67

DDYDDDL

Subject: 189 DDYDDDL 195

Score = 40 (18.7 bits), Expect = 6.2e-09, Sum P(2) = 6.2e-09
Identities = 7/11 (63%), Positives = 10/11 (90%)

Query: 1 SSQYRGVTFYR 11

SS+YRGVT ++

Subject: 221 SSKYRGVTLHK 231

Score = 114 (53.2 bits), Expect = 6.2e-09, Sum P(2) = 6.2e-09
Identities = 25/43 (58%), Positives = 30/43 (69%)

Query: 25 KQVYLGFFDTAHAARAYDRAAIKFRGVEADINFNIDDDYDDDL 67
K VYLG FDT AARAYD+AAIK G +A NF+ YD++L

Subject: 246 KYVYLGFLFDTEVEAARAYDAAIKCNGKDAVTNFDPSIYDEEL 288

gi|2944040 (AF048900) indeterminate spikelet 1 [Zea mays]
Length = 433

Score = 345 (161.1 bits), Expect = 1.9e-40, P = 1.9e-40
Identities = 61/67 (91%), Positives = 66/67 (98%)

Query: 1 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAARAYDRAAIKFRGVEADINFNI 60
SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAARAYDRAAIKFRG++ADINF++

Subject: 110 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAARAYDRAAIKFRGLDADINFSL 169

Query: 61 DDYDDDL 67
DY+DDL

Subject: 170 SDYEDDL 176

Score = 40 (18.7 bits), Expect = 7.7e-08, Sum P(2) = 7.7e-08
Identities = 7/11 (63%), Positives = 10/11 (90%)

Query: 1 SSQYRGVTFYR 11

SS+YRGVT ++

Subject: 202 SSKYRGVTLHK 212

Score = 106 (49.5 bits), Expect = 7.7e-08, Sum P(2) = 7.7e-08
Identities = 22/40 (55%), Positives = 27/40 (67%)

Query: 25 KQVYLGFFDTAHAARAYDRAAIKFRGVEADINFNIDDDYD 64
K +YLG FD+ AARAYDRAA++F G EA NF Y+

Subject: 227 KYIYLGFLFDSEVEAARAYDRAALRFNGREAVTNFEPSSYN 266

gi|2281639 (AF003100) AP2 domain containing protein RAP2.7 [Arabidopsis thaliana]
Length = 403

Score = 340 (158.7 bits), Expect = 9.5e-40, P = 9.5e-40
Identities = 60/67 (89%), Positives = 65/67 (97%)

Query: 1 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAARAYDRAAIKFRGVEADINFNI 60

Sbjct: 105 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAARAYDRAAIKFRGV+ADINF +
164

Query: 61 DDYDDDL 67
DY++D+

Sbjct: 165 GDYEEDM 171

Score = 40 (18.7 bits), Expect = 0.017, Sum P(2) = 0.017
Identities = 7/11 (63%), Positives = 10/11 (90%)

Query: 1 SSQYRGVTYR 11
SS+YRGVT ++

Sbjct: 197 SSKYRGVTLHK 207

Score = 64 (29.9 bits), Expect = 0.017, Sum P(2) = 0.017
Identities = 12/28 (42%), Positives = 18/28 (64%)

Query: 40 RAYDRAAIKFRGVEADINFNIDDDYDDDL 67
+AYD+AAI G EA NF + Y +++

Sbjct: 222 KAYDKAAINTNGREAVTNFEMSSYQNEI 249

gi|1732031 (U41466) AP2 DNA-binding domain protein [Zea mays]
Length = 446

Score = 327 (152.7 bits), Expect = 6.4e-38, P = 6.4e-38
Identities = 58/67 (86%), Positives = 63/67 (94%)

Query: 1 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAARAYDRAAIKFRGVEADINFNI 60

SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTA AAARAYD+AAIKFRG+ ADINF +

Sbjct: 111 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAQAAARAYDQAAIKFRGLNADINFTL 170

Query: 61 DDYDDDL 67
DDY D++

Sbjct: 171 DDYKDEM 177

Score = 111 (51.8 bits), Expect = 1.5e-07, P = 1.5e-07
Identities = 24/43 (55%), Positives = 29/43 (67%)

Query: 25 KQVYLGGFDTAHAARAYDRAAIKFRGVEADINFNIDDDYDDDL 67

K VYLG +DT AA+AYD+AAIK G EA NF+ YD +L

Sbjct: 228 KYVYLGLYDTETEAAQAYDKAAIKCYGKEAVTNFDAQSYDKEL 270

gi|3402680 (AC004697) putative floral homeotic protein [Arabidopsis thaliana]
Length = 236

Score = 319 (148.9 bits), Expect = 8.5e-37, P = 8.5e-37
Identities = 56/67 (83%), Positives = 62/67 (92%)

Query: 1 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAARAYDRAAIKFRGVEADINFNI 60

SS YRGVTFYRRTGRWESHIWDCGKQVYLGGFDTA+ AARAYDRAAI+FRG++ADINF +

Sbjct: 106 SSHYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAYTAARAYDRAAIRFRGLQADINFIV 165

Query: 61 DDYDDDL 67

DDY D+

Sbjct: 166 DDYKQDI 172

gi|2098818 (AF001012) GLOSSY15 [Zea mays]
Length = 139

Score = 33 (15.4 bits), Expect = 2.0e-09, Sum P(3) = 2.0e-09
Identities = 6/11 (54%), Positives = 10/11 (90%)

Query: 1 SSQYRGVTFYR 11
SS++RGVT ++
Sbjct: 72 SSRFRGVTQHK 82

Score = 30 (14.0 bits), Expect = 2.0e-09, Sum P(3) = 2.0e-09
Identities = 4/9 (44%), Positives = 7/9 (77%)

Query: 12 RTGRWESHI 20
+ G+WE+ I
Sbjct: 82 KCGKWEARI 90

Score = 111 (51.8 bits), Expect = 2.0e-09, Sum P(3) = 2.0e-09
Identities = 24/43 (55%), Positives = 29/43 (67%)

Query: 25 KQVYLGFDATAHAAARAYDRAAIKFRGVEADINFNIDDDYDDDL 67
K VYLG +DT AA+AYD+AAIK G EA NF+ YD +L
Sbjct: 97 KYVYLGLYDTETEAAQAYDKAAIKCYGKEAVTNFDAQSYDKEL 139

Score = 205 (95.7 bits), Expect = 9.0e-21, P = 9.0e-21
Identities = 37/46 (80%), Positives = 42/46 (91%)

Query: 22 DCGKQVYLGFDATAHAAARAYDRAAIKFRGVEADINFNIDDDYDDDL 67
DCGKQVYLGFDATA AAARAYD+AAIKFRG+ ADINF +DDY D++
Sbjct: 1 DCGKQVYLGFDATAQAAARAYDQAAIKFRGLNADINFTRDDYKDEM 46

gi|2887500 (AC002339) putative AP2 domain-containing protein
[Arabidopsis thaliana]
Length = 436

Score = 84 (39.2 bits), Expect = 1.3e-16, Sum P(2) = 1.3e-16
Identities = 15/22 (68%), Positives = 19/22 (86%)

Query: 1 SSQYRGVTFYRRTGRWESHIWD 22
SS YRGVT +R TGR+E+H+WD
Sbjct: 68 SSIYRGVTRHRWTGRYEAHLWD 89

Score = 126 (58.8 bits), Expect = 1.3e-16, Sum P(2) = 1.3e-16
Identities = 27/52 (51%), Positives = 32/52 (61%)

Query: 16 WESHIWDCGKQVYLGFDATAHAAARAYDRAAIKFRGVEADINFNIDDDYDDDL 67
W + GKQVYLG +D AAARAYD AA+K+ G INF + DY DL
Sbjct: 93 WNQNQNKKKGKQVYLGAYDDEEAAARAYDLAALKYWGPGLINFPVTDYTRDL 144

pir||S71365 AP2 domain-containing protein - Arabidopsis thaliana
gi|1209099 (U40256) AINTEGUMENTA [Arabidopsis thaliana] gi|1244708
(U41339) ANT [Arabidopsis thaliana]
Length = 555

Score = 89 (41.6 bits), Expect = 6.6e-16, Sum P(2) = 6.6e-16
Identities = 15/22 (68%), Positives = 20/22 (90%)

Query: 1 SSQYRGVTFYRRTGRWESHIWD 22
+SQYRGVT +R TGR+E+H+WD
Sbjct: 281 TSQYRGVTRHRWTGRYE AHLWD 302

Score = 116 (54.2 bits), Expect = 6.6e-16, Sum P(2) = 6.6e-16
Identities = 21/44 (47%), Positives = 30/44 (68%)

Query: 24 GKQVYLGGFDTAHAARAYDRAAIKFRGVEADINFNIDDD 67
G+QVYLGG+D AARAYD AA+K+ G NF+ ++Y ++
Sbjct: 314 GRQVYLGGYDMEEKAARAYDLAALKYWGPSTHTNFSQENYQKEI 357

Score = 56 (26.1 bits), Expect = 3.1e-11, Sum P(2) = 3.1e-11
Identities = 10/20 (50%), Positives = 15/20 (75%)

Query: 1 SSQYRGVTFYRRTGRWESHI 20
+S YRGVT + + GRW++ I
Sbjct: 383 ASIYRGVTRHHQHGRWQARI 402

Score = 115 (53.7 bits), Expect = 3.1e-11, Sum P(2) = 3.1e-11
Identities = 25/42 (59%), Positives = 27/42 (64%)

Query: 25 KQVYLGGFDTAHAARAYDRAAIKFRGVEADINFNIDDD 66
K +YLG F T AA AYD AAIKFRG A NF+I YD D
Sbjct: 409 KDLYLGTFGTQEEAAEAYDVAAIKFRGTONAVTNFDITRYDVD 450

gi|1171429 (U44028) CKC [Arabidopsis thaliana]
Length = 555

Score = 89 (41.6 bits), Expect = 6.6e-16, Sum P(2) = 6.6e-16
Identities = 15/22 (68%), Positives = 20/22 (90%)

Query: 1 SSQYRGVTFYRRTGRWESHIWD 22
+SQYRGVT +R TGR+E+H+WD
Sbjct: 281 TSQYRGVTRHRWTGRYE AHLWD 302

Score = 116 (54.2 bits), Expect = 6.6e-16, Sum P(2) = 6.6e-16
Identities = 21/44 (47%), Positives = 30/44 (68%)

Query: 24 GKQVYLGGFDTAHAARAYDRAAIKFRGVEADINFNIDDD 67
G+QVYLGG+D AARAYD AA+K+ G NF+ ++Y ++
Sbjct: 314 GRQVYLGGYDMEEKAARAYDLAALKYWGPSTHTNFSQENYQKEI 357

Score = 56 (26.1 bits), Expect = 3.1e-11, Sum P(2) = 3.1e-11
Identities = 10/20 (50%), Positives = 15/20 (75%)

Query: 1 SSQYRGVTFYRRTGRWESHI 20
+S YRGVT + + GRW++ I
Sbjct: 383 ASIYRGVTRHHQHGRWQARI 402

Score = 115 (53.7 bits), Expect = 3.1e-11, Sum P(2) = 3.1e-11
Identities = 25/42 (59%), Positives = 27/42 (64%)

Query: 25 KQVYLGGFDTAHAARAYDRAAIKFRGVEADINFNIDDD 66
K +YLG F T AA AYD AAIKFRG A NF+I YD D
Sbjct: 409 KDLYLGTFGTQEEAAEAYDVAAIKFRGTONAVTNFDITRYDVD 450

gnl|PID|e1188628 (Z47554) orf [Zea mays]
Length = 485

Score = 77 (36.0 bits), Expect = 3.2e-15, Sum P(2) = 3.2e-15
Identities = 13/22 (59%), Positives = 19/22 (86%)

Query: 1 SSQYRGVTFYRRTGRWESHIWD 22
+S YRGVT +R TGR+E+H+W+
Sbjct: 138 TSIYRGVTRHRWTGRYEAHLWE 159

Score = 123 (57.4 bits), Expect = 3.2e-15, Sum P(2) = 3.2e-15
Identities = 23/44 (52%), Positives = 30/44 (68%)

Query: 24 GKQVYLGFFDTAHAARAYDRAAIKFRGVEADINFNIDDDYDDL 67
G+QVYLG+D AARAYD AA+KF G NF + +Y+ +L
Sbjct: 171 GRQVYLGGYDKEEKAARAYDLAALKFWGPTTTNFQVSNEYKEL 214

Score = 56 (26.1 bits), Expect = 5.4e-10, Sum P(2) = 5.4e-10
Identities = 10/20 (50%), Positives = 15/20 (75%)

Query: 1 SSQYRGVTFYRRTGRWESHI 20
+S YRGVT + + GRW++ I
Sbjct: 240 ASIYRGVTRHHQHGRWQARI 259

Score = 106 (49.5 bits), Expect = 5.4e-10, Sum P(2) = 5.4e-10
Identities = 22/40 (55%), Positives = 26/40 (65%)

Query: 25 KQVYLGFFDTAHAARAYDRAAIKFRGVEADINFNIDDDYD 64
K +YLG F T AA AYD AAIKFRG+ A N ++ YD
Sbjct: 266 KDLYLGTFSTQEEAAEAYDIAAIKFRGLNAVTNLDMSRYD 305

pir||S54116 hypothetical protein - maize
Length = 485

Score = 71 (33.2 bits), Expect = 0.061, P = 0.059
Identities = 12/26 (46%), Positives = 19/26 (73%)

Query: 1 SSQYRGVTFYRRTGRWESHIWDCGKQ 26
+S YRGVT + + GRW++ I CG++
Sbjct: 240 ASIYRGVTRHHQHGRWQARIQCGRK 265

Score = 123 (57.4 bits), Expect = 3.0e-09, P = 3.0e-09
Identities = 23/44 (52%), Positives = 30/44 (68%)

Query: 24 GKQVYLGFFDTAHAARAYDRAAIKFRGVEADINFNIDDDYDDL 67
G+QVYLG+D AARAYD AA+KF G NF + +Y+ +L
Sbjct: 171 GRQVYLGGYDKEEKAARAYDLAALKFWGPTTTNFQVSNEYKEL 214

gi|2281641 (AF003101) AP2 domain containing protein RAP2.8 [Arabidopsis thaliana]
Length = 334

Score = 112 (52.3 bits), Expect = 1.1e-07, P = 1.1e-07

Identities = 24/54 (44%), Positives = 35/54 (64%)

Query: 14 GRWESHIWDCGKQVYLGFFDTAHHAAARAYDRAAIKFRGVEADINFNIDDYDDDL 67

GRW + I++ +V+LG F+ AAR+YD AA +FRG +A +NF D DL

Sbjct: 56 GRWGAQIYEKHQRWLGTNEQEEAARSYDIAACRFRGRDAVVNFKNVLEDGDL 109

gi|2281637 (AF003099) AP2 domain containing protein RAP2.6 [Arabidopsis thaliana]
Length = 164

Score = 110 (51.4 bits), Expect = 2.0e-07, P = 2.0e-07

Identities = 21/33 (63%), Positives = 28/33 (84%)

Query: 26 QVYLGGFDTAHHAAARAYDRAAIKFRGVEADINF 58

+V+LG F+TA AAARAYD AA++FRG +A +NF

Sbjct: 56 RVWLGTTFETAEAAARAYDAAALRFRGSKAKLNF 88

gnl|PID|d1007901 (D38125) EREBP-4 [Nicotiana tabacum]
Length = 291

Score = 110 (51.4 bits), Expect = 2.0e-07, P = 2.0e-07

Identities = 22/38 (57%), Positives = 29/38 (76%)

Query: 24 GKQVYLGGFDTAHHAAARAYDRAAIKFRGVEADINFID 61

G +V+LG FDTA AA+AYDRAA K RG +A +NF ++

Sbjct: 167 GTRVWLGTFTDAIEAAKAYDRAAFKLRGSKAIVNFPLE 204

gi|3617742 (AC005687) RAP2.6 [Arabidopsis thaliana]
Length = 192

Score = 110 (51.4 bits), Expect = 2.0e-07, P = 2.0e-07

Identities = 21/33 (63%), Positives = 28/33 (84%)

Query: 26 QVYLGGFDTAHHAAARAYDRAAIKFRGVEADINF 58

+V+LG F+TA AAARAYD AA++FRG +A +NF

Sbjct: 84 RVWLGTTFETAEAAARAYDAAALRFRGSKAKLNF 116

gi|1903358 (AC000104) Similar to Nicotiana EREBP-3 (gb|D38124).
[Arabidopsis thaliana]
Length = 133

Score = 106 (49.5 bits), Expect = 7.4e-07, P = 7.4e-07

Identities = 22/35 (62%), Positives = 26/35 (74%)

Query: 24 GKQVYLGGFDTAHHAAARAYDRAAIKFRGVEADINF 58

G++V+LG FDTA AARAYDRAA RG A +NF

Sbjct: 42 GERVWLGTFTDAEDAARAYDRAAYSMRGKAAILNF 76

gnl|PID|d1033384 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]

Length = 300

Score = 105 (49.0 bits), Expect = 1.0e-06, P = 1.0e-06
Identities = 21/38 (55%), Positives = 28/38 (73%)

Query: 24 GKQVYLGFDATAHAAARAYDRAAIKFRGVEADINFID 61
G +V+LG FDTA AARAYD AA + RG +A +NF ++
Sbjct: 178 GSRVWLGTFDATAEAAARAYDEAAFRRLRGSKAILNFPLE 215

gi|2529675 (AC002535) putative AP2 domain containing protein
[Arabidopsis thaliana]
Length = 171

Score = 31 (14.5 bits), Expect = 1.1e-06, Sum P(2) = 1.1e-06
Identities = 7/17 (41%), Positives = 9/17 (52%)

Query: 11 RRTGRWESHIWDCGKQV 27
R G+W + I D K V
Sbjct: 56 RPWGKWAEEIRDPSKGV 72

Score = 101 (47.2 bits), Expect = 1.1e-06, Sum P(2) = 1.1e-06
Identities = 22/35 (62%), Positives = 26/35 (74%)

Query: 24 GKQVYLGFDATAHAAARAYDRAAIKFRGVEADINF 58
G +V+LG F TA AARAYD AAIK RG +A +NF
Sbjct: 71 GVRVWLGTFKTADEAAARAYDVAAIKIRGRKAKLNF 105

gi|2281635 (AF003098) AP2 domain containing protein RAP2.5 [Arabidopsis thaliana]
Length = 213

Score = 30 (14.0 bits), Expect = 2.7e-06, Sum P(2) = 2.7e-06
Identities = 7/16 (43%), Positives = 10/16 (62%)

Query: 11 RRTGRWESHIWDCGKQ 26
R GR+ + I D GK+
Sbjct: 31 RPWGRYAAEIRDPGKK 46

Score = 100 (46.7 bits), Expect = 2.7e-06, Sum P(2) = 2.7e-06
Identities = 21/33 (63%), Positives = 24/33 (72%)

Query: 26 QVYLGGFDATAHAAARAYDRAAIKFRGVEADINF 58
+V+LG FDTA AARAYD AA FRG +A NF
Sbjct: 48 RVWLGTFDATAEEAARAYDTAARDFRGAKAKTNF 80

gnl|PID|d1033383 (AB008106) ethylene responsive element binding factor
4 [Arabidopsis thaliana]
Length = 222

Score = 30 (14.0 bits), Expect = 2.8e-06, Sum P(2) = 2.8e-06
Identities = 7/16 (43%), Positives = 10/16 (62%)

Query: 11 RRTGRWESHIWDCGKQ 26
R GR+ + I D GK+

Sbjct: 31 RPWGRYAAEIRDPGKK 46

Score = 100 (46.7 bits), Expect = 2.8e-06, Sum P(2) = 2.8e-06
Identities = 21/33 (63%), Positives = 24/33 (72%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58

+V+LG FDTA AARAYD AA FRG +A NF

Sbjct: 48 RVWLGTTFDTAEEAARAYDTAARDFRGAKAKTNF 80

gi|1707016 (U78721) cadmium-induced protein isolog [Arabidopsis thaliana]
Length = 218

Score = 101 (47.2 bits), Expect = 3.7e-06, P = 3.7e-06
Identities = 20/33 (60%), Positives = 26/33 (78%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58

+V+LG FDTA AA AYD+AA +FRG +A +NF

Sbjct: 93 RVWLGTTFDTAEEAALAYDKAAFEFRGHKAKLNF 125

gi|2281629 (AF003095) AP2 domain containing protein RAP2.2 [Arabidopsis thaliana]
Length = 246

Score = 101 (47.2 bits), Expect = 3.7e-06, P = 3.7e-06
Identities = 20/35 (57%), Positives = 25/35 (71%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58

G + +LG FDTA AARAYD AA + RG +A +NF

Sbjct: 16 GSREWLGTTFDTAEEAARAYDAAARRIRGKAKVNF 50

gi|2213783 (U89256) Pt15 [Lycopersicon esculentum]
Length = 161

Score = 100 (46.7 bits), Expect = 5.1e-06, P = 5.1e-06
Identities = 20/35 (57%), Positives = 26/35 (74%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58

G +V+LG F+TA AA AYDRAA + RG +A +NF

Sbjct: 81 GARVWLGTTFETAAALAYDRAAFMRGAKALLNF 115

gnl|PID|d1007900 (D38124) EREBP-3 [Nicotiana tabacum]
Length = 225

Score = 30 (14.0 bits), Expect = 7.3e-06, Sum P(2) = 7.3e-06
Identities = 7/16 (43%), Positives = 10/16 (62%)

Query: 11 RRTGRWESHIWDCGKQ 26

R GR+ + I D GK+

Sbjct: 33 RPWGRYAAEIRDPGKK 48

Score = 97 (45.3 bits), Expect = 7.3e-06, Sum P(2) = 7.3e-06
Identities = 20/33 (60%), Positives = 25/33 (75%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
+V+LG FDTA AA+AYD AA +FRG +A NF
Sbjct: 50 RVWLGTFTDAEEAKAYDTAAREFRGPKAKTNF 82

gi|1732406 (U81157) S25-XP1 DNA binding protein [Nicotiana tabacum]
Length = 277

Score = 98 (45.8 bits), Expect = 9.8e-06, P = 9.8e-06
Identities = 20/44 (45%), Positives = 28/44 (63%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNIDDD 67
G +V+LG FD+ AAA AYD+AA RG A +NF ++ + L
Sbjct: 114 GVRVWLGTFTDSPEAAALAYDQAAFLMRGTSAILNFPVETVQESL 157

gi|3600050 (AF080120) contains similarity to AP2 domain containing
proteins [Arabidopsis thaliana]
Length = 287

Score = 31 (14.5 bits), Expect = 1.3e-05, Sum P(2) = 1.3e-05
Identities = 6/17 (35%), Positives = 10/17 (58%)

Query: 11 RRTGRWESHIWDCGKQV 27
R G+W + I D ++V
Sbjct: 93 RPWGKWAEEIRDPSRRV 109

Score = 95 (44.4 bits), Expect = 1.3e-05, Sum P(2) = 1.3e-05
Identities = 19/33 (57%), Positives = 24/33 (72%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
+V+LG FDTA AA YD AAI+ RG A++NF
Sbjct: 110 RVWLGTFTDAEEAIIVYDNAAIQLRGPNELNF 142

gnl|PID|d1032484 (AB013301) ethylene responsive element binding factor
[Arabidopsis thaliana]
Length = 281

Score = 97 (45.3 bits), Expect = 1.4e-05, P = 1.4e-05
Identities = 19/38 (50%), Positives = 28/38 (73%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNID 61
G +V+LG F+TA AARAYD+ A + RG +A +NF ++
Sbjct: 159 GTRVWLGTFTATAEAAAYDKEAFRLRGSKAILNFPLE 196

gnl|PID|d1033382 (AB008105) ethylene responsive element binding factor
3 [Arabidopsis thaliana]
Length = 225

Score = 97 (45.3 bits), Expect = 1.4e-05, P = 1.4e-05
Identities = 21/36 (58%), Positives = 25/36 (69%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNID 61

+V+LG FD+A AARAYD AA RG +A NF ID
Sbjct: 51 RVWLGTFDSEAARAYDSAARNLRGPKAKTNFPID 86

gnl|PID|e327065 (297343) EREBP-4 homolog [Arabidopsis thaliana]
Length = 603

Score = 97 (45.3 bits), Expect = 1.4e-05, P = 1.4e-05
Identities = 19/38 (50%), Positives = 28/38 (73%)

Query: 24 GKQVYLGGFDTAHAARAYDRAAIKFRGVEADINFNID 61
G +V+LG F+TA AARAYD+ A + RG +A +NF ++
Sbjct: 159 GTRVWLGTFETAIARAYDKEAFRLRGSKAILNFPLE 196

gi|2213785 (U89257) Pt16 [Lycopersicon esculentum]
Length = 248

Score = 30 (14.0 bits), Expect = 1.5e-05, Sum P(2) = 1.5e-05
Identities = 6/12 (50%), Positives = 7/12 (58%)

Query: 11 RRTGRWESHIWD 22
R GRW + I D
Sbjct: 104 RPWGRWAAEIRD 115

Score = 95 (44.4 bits), Expect = 1.5e-05, Sum P(2) = 1.5e-05
Identities = 18/37 (48%), Positives = 26/37 (70%)

Query: 24 GKQVYLGGFDTAHAARAYDRAAIKFRGVEADINFNI 60
GK+V+LG +DT AA YD+AA+K +G +A NF +
Sbjct: 119 GKRVWLGYDTPEAAVYDKAAVKLKGPDAVTNFPV 155

gi|2281649 (AF003105) AP2 domain containing protein RAP2.12
[Arabidopsis thaliana]
Length = 317

Score = 96 (44.8 bits), Expect = 1.9e-05, P = 1.9e-05
Identities = 19/35 (54%), Positives = 25/35 (71%)

Query: 24 GKQVYLGGFDTAHAARAYDRAAIKFRGVEADINF 58
G ++++LG F TA AARAYD AA + RG +A +NF
Sbjct: 105 GARIWLGTFKTAAEAARAYDAAARRIRGSKAKVNF 139

gnl|PID|d1033380 (AB008103) ethylene responsive element binding factor
1 [Arabidopsis thaliana]
Length = 266

Score = 96 (44.8 bits), Expect = 1.9e-05, P = 1.9e-05
Identities = 20/35 (57%), Positives = 25/35 (71%)

Query: 24 GKQVYLGGFDTAHAARAYDRAAIKFRGVEADINF 58
G +V+LG F+TA AA AYDRAA + RG A +NF
Sbjct: 168 GARVWLGTFETAEADAALAYDRAAFRMGRGSRALLNF 202

gi|3342211 (U89255) Pt14 [Lycopersicon esculentum]
Length = 234

Score = 93 (43.4 bits), Expect = 4.9e-05, P = 4.9e-05
Identities = 18/35 (51%), Positives = 26/35 (74%)

Query: 24 GKQVYLGGFDTAHAARAYDRAAIKFRGVEADINF 58
G +V+LG ++TA AA AYD+AA + RG +A +NF
Sbjct: 128 GARVWLGTYETAAIAAYDKAAYRMRGSKAHLNF 162

gi|3264767 (AF071893) AP2 domain containing protein [Prunus armeniaca]
Length = 280

Score = 93 (43.4 bits), Expect = 4.9e-05, P = 4.9e-05
Identities = 19/35 (54%), Positives = 25/35 (71%)

Query: 24 GKQVYLGGFDTAHAARAYDRAAIKFRGVEADINF 58
G +V+LG F+TA AARAYD A + RG +A +NF
Sbjct: 33 GVRVWLGTNTAEEAARAYDSEARRIRGKKAKVNF 67

gi|3065895 (AF058827) TSI1 [Nicotiana tabacum]
Length = 251

Score = 30 (14.0 bits), Expect = 5.4e-05, Sum P(2) = 5.4e-05
Identities = 6/12 (50%), Positives = 7/12 (58%)

Query: 11 RRTGRWESHIWD 22
R GRW + I D
Sbjct: 113 RPWGRWAAEIRD 124

Score = 91 (42.5 bits), Expect = 5.4e-05, Sum P(2) = 5.4e-05
Identities = 18/35 (51%), Positives = 24/35 (68%)

Query: 24 GKQVYLGGFDTAHAARAYDRAAIKFRGVEADINF 58
GK+V+LG +DT AA YD AA+K +G +A NF
Sbjct: 128 GKRVWLGTYDTPEEAAIVYDAAAVALKGPDAVTNF 162

gi|1688233 (U77655) DNA binding protein homolog [Solanum tuberosum]
Length = 298

Score = 32 (14.9 bits), Expect = 8.0e-05, Sum P(3) = 8.0e-05
Identities = 7/17 (41%), Positives = 10/17 (58%)

Query: 11 RRTGRWESHIWDCGKQV 27
R G+W + I D K+V
Sbjct: 75 RPWGKWAEEIRDPRKRV 91

Score = 39 (18.2 bits), Expect = 8.0e-05, Sum P(3) = 8.0e-05
Identities = 8/13 (61%), Positives = 11/13 (84%)

Query: 26 QVYLGGFDTAHA 38
+V+LG F+TA AA

Sbjct: 92 RVWLGTFTNTAEAA 104

Score = 74 (34.6 bits), Expect = 8.0e-05, Sum P(3) = 8.0e-05
Identities = 16/27 (59%), Positives = 19/27 (70%)

Query: 38 AARAYDRAAIKFRGVEADINFNIDDYD 64
AARAYDR A K RG +A +NF +D D
Sbjct: 103 AARAYDREARKIRGKKAKVNFPNEDDD 129

gnl|PID|d1007902 (D38126) EREBP-2 [Nicotiana tabacum]
Length = 233

Score = 91 (42.5 bits), Expect = 9.5e-05, P = 9.5e-05
Identities = 18/35 (51%), Positives = 26/35 (74%)

Query: 24 GKQVYLGGFDTAHAARAYDRAAIKFRGVEADINF 58
G +V+LG ++TA AA AYD+AA + RG +A +NF
Sbjct: 121 GARVWLGTYETEEAALAYDKAAYRMRGSKALLNF 155

gi|2344900 (AC002388) EREBP isolog [Arabidopsis thaliana]
Length = 226

Score = 90 (42.0 bits), Expect = 0.00013, P = 0.00013
Identities = 18/35 (51%), Positives = 25/35 (71%)

Query: 24 GKQVYLGGFDTAHAARAYDRAAIKFRGVEADINF 58
G +V+LG ++T AA AYDAA + RG +A +NF
Sbjct: 114 GARVWLGTYETPEDAAVAYDRAAFQLRGSKAKLNF 148

gi|2281633 (AF003097) AP2 domain containing protein RAP2.4 [Arabidopsis thaliana]
Length = 229

Score = 90 (42.0 bits), Expect = 0.00013, P = 0.00013
Identities = 19/33 (57%), Positives = 24/33 (72%)

Query: 26 QVYLGGFDTAHAARAYDRAAIKFRGVEADINF 58
+++LG FDTA AA AYD+AA K RG A +NF
Sbjct: 70 RLWLGTFTAEAAALAYDKAAYKLRGDFARLN 102

gnl|PID|d1033381 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
Length = 243

Score = 88 (41.1 bits), Expect = 0.00025, P = 0.00025
Identities = 19/35 (54%), Positives = 24/35 (68%)

Query: 24 GKQVYLGGFDTAHAARAYDRAAIKFRGVEADINF 58
G +V+LG F+TA AA AYD AA + RG A +NF
Sbjct: 139 GARVWLGTFTAEADAALAYDIAAFMRGSRALLNF 173

gnl|PID|e1287891 (AL022605) putative protein [Arabidopsis thaliana]
Length = 272

Score = 88 (41.1 bits), Expect = 0.00025, P = 0.00025
Identities = 19/33 (57%), Positives = 23/33 (69%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
+++LG FDTA AA AYD AA K RG A +NF
Sbjct: 116 RLWLGTTFDTAEEAAMAYDLAAYKLRGEFARLNF 148

gnl|PID|e353340 (AJ001911) putative Ckc2 [Arabidopsis thaliana]
Length = 246

Score = 88 (41.1 bits), Expect = 0.00025, P = 0.00025
Identities = 19/35 (54%), Positives = 25/35 (71%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
G +V+LG F+TA AA AYD AA + RG +A +NF
Sbjct: 101 GVRVWLGTTFNTAEEAAMAYDVAAKQIRGEKAKLNF 135

gi|2281631 (AF003096) AP2 domain containing protein RAP2.3 [Arabidopsis thaliana]
Length = 248

Score = 87 (40.6 bits), Expect = 0.00035, P = 0.00034
Identities = 19/35 (54%), Positives = 25/35 (71%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
G +V+LG F+TA AA AYD AA + RG +A +NF
Sbjct: 100 GVRVWLGTTFNTAEEAAMAYDVAAKQIRGDKAKLNF 134

gnl|PID|d1007899 (D38123) ERF1 [Nicotiana tabacum]
Length = 236

Score = 87 (40.6 bits), Expect = 0.00035, P = 0.00034
Identities = 17/35 (48%), Positives = 25/35 (71%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
G +V+LG ++T AA AYD+AA + RG +A +NF
Sbjct: 127 GARVWLGTYETDEAAIAAYDKAAYRMRGSKAHLNF 161

gnl|PID|e1283534 (AL022197) transcriptional activator CBF1 [Arabidopsis thaliana]
gnl|PID|d1034401 (AB013816) DREB1B [Arabidopsis thaliana]
gnl|PID|d1034764 (AB007788) DREB1B [Arabidopsis thaliana]
Length = 213

Score = 32 (14.9 bits), Expect = 0.00039, Sum P(2) = 0.00039
Identities = 5/16 (31%), Positives = 10/16 (62%)

Query: 11 RRTGRWESHIWDCGKQ 26
R +G+W S + + K+

Sbjct: 54 RNSGKWWSEVREPNKK 69

Score = 82 (38.3 bits), Expect = 0.00039, Sum P(2) = 0.00039
Identities = 17/33 (51%), Positives = 23/33 (69%)

Query: 26 QVYLGFFDTAHAAARAYDRAAIKFRGVEADINF 58

+++LG F TA AARA+D AA+ RG A +NF

Sbjct: 71 RIWLGTQTAEMAAARAHDVAALALRGRSACLNF 103

gi|1899058 (U77378) transcriptional activator CBF1 [Arabidopsis thaliana]
Length = 213

Score = 32 (14.9 bits), Expect = 0.00039, Sum P(2) = 0.00039
Identities = 5/16 (31%), Positives = 10/16 (62%)

Query: 11 RRTGRWESHIWDCGKQ 26

R +G+W S + + K+

Sbjct: 54 RNSGKWWSEVREPNKK 69

Score = 82 (38.3 bits), Expect = 0.00039, Sum P(2) = 0.00039
Identities = 17/33 (51%), Positives = 23/33 (69%)

Query: 26 QVYLGFFDTAHAAARAYDRAAIKFRGVEADINF 58

+++LG F TA AARA+D AA+ RG A +NF

Sbjct: 71 RIWLGTQTAEMAAARAHDVAALALRGRSACLNF 103

gi|2281643 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
Length = 94

Score = 86 (40.2 bits), Expect = 0.00048, P = 0.00048
Identities = 18/40 (45%), Positives = 25/40 (62%)

Query: 26 QVYLGFFDTAHAAARAYDRAAIKFRGVEADINFNIDDYDD 65

+++LG + TA AAARAYD A RG A +NF + + D

Sbjct: 3 RIWLGSYKTAVAAARAYDTAVFYLRGSPSARLNFPPEEVFKD 42

gnl|PID|e1249610 (AL021710) EREBP - like protein [Arabidopsis thaliana]
Length = 303

Score = 85 (39.7 bits), Expect = 0.00066, P = 0.00066
Identities = 16/30 (53%), Positives = 22/30 (73%)

Query: 24 GKQVYLGFFDTAHAAARAYDRAAIKFRGVE 53

G +V+LG F TA AA AYD+AA++ RG +

Sbjct: 132 GVRVWLGTQTAEEAMAYDKAAVRIRGTQ 161

gnl|PID|e353195 (Z99707) APETALA2 domain containing protein homolog [Arabidopsis thaliana]
Length = 196

Score = 29 (13.5 bits), Expect = 0.00066, Sum P(2) = 0.00066

Identities = 5/16 (31%), Positives = 10/16 (62%)

Query: 11 RRTGRWESHIWDCGKQ 26
R+ G+W + I + K+
Sbjct: 36 RKWGKWWVAEIREPNKR 51

Score = 83 (38.8 bits), Expect = 0.00066, Sum P(2) = 0.00066
Identities = 16/33 (48%), Positives = 21/33 (63%)

Query: 26 QVYLGFFDTAHAARAYDRAAIKFRGVEADINF 58
+++LG + T AAARAYD A RG A +NF
Sbjct: 53 RIWLGSYSTPEAAARAYDTAVFYLRGSPSARLN 85

gi|2281647 (AF003104) AP2 domain containing protein RAP2.11
[Arabidopsis thaliana]
Length = 255

Score = 31 (14.5 bits), Expect = 0.00090, Sum P(2) = 0.00090
Identities = 5/17 (29%), Positives = 11/17 (64%)

Query: 11 RRTGRWESHIWDCGKQV 27
R +G+W + I D +++
Sbjct: 30 RPSGKWWVAEIKDTTQKI 46

Score = 81 (37.8 bits), Expect = 0.00090, Sum P(2) = 0.00090
Identities = 17/33 (51%), Positives = 21/33 (63%)

Query: 26 QVYLGFFDTAHAARAYDRAAIKFRGVEADINF 58
+++LG F+TA AAARAYD AA RG NF
Sbjct: 47 RMWLGTTFETAEAAARAYDEAACLLRGSNTRTNF 79

Parameters:

V=100
B=50
H=0

Lambda K H
0.324 0.140 0.453

Cutoff to enter 2nd pass: >= 38 (0.0 bits)

E	S	T1	T2	X1	X2	W	Gap	
10.0	59	11	11		-15	-22	40	50

Database: Non-redundant GenBank CDS translations+PDB+SwissProt+SPupdate+PIR
Posted date: Oct 22, 1998 7:43 AM
of letters in database: 101,007,400
of sequences in database: 331,304

Number of Hits to DB: 1st pass: 14105114, 2nd pass: 228077
Number of Sequences: 1st pass: 331304, 2nd pass: 2078
Number of extensions: 1st pass: 447103, 2nd pass: 171014
Number of successful extensions: 1st pass: 2078, 2nd pass: 2859
Number of sequences better than 10: 80

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